

SEQUENCE LISTING

<110> Fletcher, Jonathan A.  
Kroll, Todd G.

<120> PAX8-PPARgamma NUCLEIC ACID MOLECULES  
AND POLYPEPTIDES AND USES THEREOF

<130> B0801/7196 (ERP/MAT)

<150> US 60/177,109  
<151> 2000-01-20

<150> US 60/225,079  
<151> 2000-08-14

<160> 47

<170> FastSEQ for Windows Version 3.0

<210> 1  
<211> 2334  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (1)...(2334)

<400> 1

atg cct cac aac tcc atc aga tct ggc cat gga ggg ctg aac cag ctg 48  
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu  
1 5 10 15

gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg gtc cgc cag 96  
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
20 25 30

cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc gac atc tct 144  
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
35 40 45

cgc cag ctc cgc gtc agc cat ggc tgc gtc agc aag atc ctt ggc agg 192  
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
50 55 60

tac tac gag act ggc agc atc cgg cct gga gtg ata ggg ggc tcc aag 240  
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
65 70 75 80

ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa 288  
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
85 90 95

cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac cgg ctc ctg Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu 100 105 110	336
gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc agc tcc att Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile 115 120 125	384
aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac ctc cct atg Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met 130 135 140	432
gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac acg ctg atc Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile 145 150 155 160	480
ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg gat tcc ctg Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu 165 170 175	528
ggc tcc acc tac tcc atc aat ggg ctc ctg ggc atc gct cag cct ggc Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly 180 185 190	576
agc gac aag agg aaa atg gat gac agt gat cag gat agc tgc cga cta Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu 195 200 205	624
agc att gac tca cag agc agc gga ccc cga aag cac ctt cgc Ser Ile Asp Ser Gln Ser Ser Ser Gly Pro Arg Lys His Leu Arg 210 215 220	672
acg gat gcc ttc agc cag cac cac ctc gag ccg ctc gag tgc cca ttt Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe 225 230 235 240	720
gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc cac acc aaa Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys 245 250 255	768
ggc gag cag ggc ctc tac ccg ctg ccc ttg ctc aac agc acc ctg gac Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp 260 265 270	816
gac ggg aag gcc acc ctg acc cct tcc aac acg cca ctg ggg cgc aac Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn 275 280 285	864
ctc tcg act cac cag acc tac ccc gtg gtg gca gaa atg acc atg gtt Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Glu Met Thr Met Val 290 295 300	912
gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val 305 310 315 320	960

gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc 1008  
Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro  
325 330 335

ttc act act gtt gac ttc tcc agc att tct act cca cat tac gaa gac 1056  
Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp  
340 345 350

att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag tat gac 1104  
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp  
355 360 365

ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct gca tct 1152  
Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser  
370 375 380

cca cct tat tat tct gag aag act cag ctc tac aat aag cct cat gaa 1200  
Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu  
385 390 395 400

gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat 1248  
Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp  
405 410 415

aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga tgc aag 1296  
Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys  
420 425 430

ggt ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt 1344  
Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys  
435 440 445

gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac 1392  
Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr  
450 455 460

tgt cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc 1440  
Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile  
465 470 475 480

agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag 1488  
Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu  
485 490 495

atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac ctc cgg 1536  
Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg  
500 505 510

gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg 1584  
Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu  
515 520 525

acc aaa gca aag gcg agg gcg atc ttg aca gga aag aca aca gac aaa 1632  
Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys  
530 535 540

tca cca ttc gtt atc tat gac atg aat tcc tta atg atg gga gaa gat Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp 545 550 555 560	1680
aaa atc aag ttc aaa cac atc acc ccc ctg cag gag cag agc aaa gag Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu 565 570 575	1728
gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala 580 585 590	1776
gtg cag gag atc aca gag tat gcc aaa agc att cct ggt ttt gta aat Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn 595 600 605	1824
ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac gag Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu 610 615 620	1872
atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu 625 630 635 640	1920
ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu 645 650 655	1968
cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val 660 665 670	2016
aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca ata ttt att Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile 675 680 685	2064
gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag Ala Val Ile Ile Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys 690 695 700	2112
ccc att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc cag Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln 705 710 715 720	2160
ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu 725 730 735	2208
cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag cta Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu 740 745 750	2256
ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg ctc Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu 755 760 765	2304

2334

<210> 2  
<211> 777  
<212> PRT  
<213> Homo Sapiens

<400> 2

Met	Pro	His	Asn	Ser	Ile	Arg	Ser	Gly	His	Gly	Gly	Leu	Asn	Gln	Leu
1				5					10					15	
Gly	Gly	Ala	Phe	Val	Asn	Gly	Arg	Pro	Leu	Pro	Glu	Val	Val	Arg	Gln
				20					25					30	
Arg	Ile	Val	Asp	Leu	Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser
						35		40				45			
Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg
						50		55			60				
Tyr	Tyr	Glu	Thr	Gly	Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys
65						70			75					80	
Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys
						85			90					95	
Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu
								105					110		
Ala	Glu	Gly	Val	Cys	Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile
						115		120				125			
Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met
130						135					140				
Asp	Ser	Cys	Val	Ala	Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile
145						150				155				160	
Pro	Ser	Ser	Ala	Val	Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu
						165			170					175	
Gly	Ser	Thr	Tyr	Ser	Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly
						180			185				190		
Ser	Asp	Lys	Arg	Lys	Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu
						195		200				205			
Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg	
210						215				220					
Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe
225						230				235				240	
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
						245			250				255		
Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
						260			265			270			
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
						275		280				285			
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Glu	Met	Thr	Met	Val
						290		295			300				
Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser	Ser	Val
305						310				315				320	
Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile	Lys	Pro
						325			330				335		
Phe	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr	Glu	Asp
						340			345			350			
Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys	Tyr	Asp

Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp

355 360 365  
Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser  
370 375 380  
Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu  
385 390 395 400  
Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp  
405 410 415  
Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys  
420 425 430  
Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys  
435 440 445  
Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr  
450 455 460  
Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile  
465 470 475 480  
Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu  
485 490 495  
Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg  
500 505 510  
Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu  
515 520 525  
Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys  
530 535 540  
Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp  
545 550 555 560  
Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu  
565 570 575  
Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala  
580 585 590  
Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn  
595 600 605  
Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu  
610 615 620  
Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu  
625 630 635 640  
Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu  
645 650 655  
Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val  
660 665 670  
Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile  
675 680 685  
Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys  
690 695 700  
Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln  
705 710 715 720  
Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu  
725 730 735  
Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu  
740 745 750  
Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu  
755 760 765  
Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
770 775

<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (1)...(2523)

<400> 3

atg cct cac aac tcc atc aga tct ggc cat gga ggg ctg aac cag ctg	48
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu	
1 5 10 15	
gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg gtc cgc cag	96
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln	
20 25 30	
cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc gac atc tct	144
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser	
35 40 45	
cgc cag ctc cgc gtc agc cat ggc tgc gtc agc aag atc ctt ggc agg	192
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
50 55 60	
tac tac gag act ggc agc atc cgg cct gga gtg ata ggg ggc tcc aag	240
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
65 70 75 80	
ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa	288
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
85 90 95	
cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac cgg ctc ctg	336
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	
100 105 110	
gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc agc tcc att	384
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile	
115 120 125	
aat aga atc cgg acc aaa gtg cag caa cca ttc aac ctc cct atg	432
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met	
130 135 140	
gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac acg ctg atc	480
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile	
145 150 155 160	
ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg gat tcc ctg	528
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu	
165 170 175	
ggc tcc acc tac tcc atc aat ggg ctc ctg ggc atc gct cag cct ggc	576
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly	
180 185 190	

agc gac aag agg aaa atg gat gac agt gat cag gat agc tgc cga cta Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu 195 200 205	624
agc att gac tca cag agc agc agc gga ccc cga aag cac ctt cgc Ser Ile Asp Ser Gln Ser Ser Ser Gly Pro Arg Lys His Leu Arg 210 215 220	672
acg gat gcc ttc agc cag cac cac ctc gag ccg ctc gag tgc cca ttt Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe 225 230 235 240	720
gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc cac acc aaa Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys 245 250 255	768
ggc gag cag ggc ctc tac ccg ctg ccc ttg ctc aac agc acc ctg gac Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Asn Ser Thr Leu Asp 260 265 270	816
gac ggg aag gcc acc ctg acc cct tcc aac acg cca ctg ggg cgc aac Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn 275 280 285	864
ctc tcg act cac cag acc tac ccc gtg gtg gca gat cct cac tca ccc Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro 290 295 300	912
ttg gcc ata aag cag gaa acc ccc gag gtg tcc agt tct agc tcc acc Leu Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Thr 305 310 315 320	960
cct tgc tct tta tct agc tcc gcc ctt ttg gat ctg cag caa gtc ggc Pro Cys Ser Leu Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly 325 330 335	1008
tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc tcc gtg tac Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr 340 345 350	1056
ggg cag ttc acg ggc cag gcc ctc tca gaa atg acc atg gtt gac Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp 355 360 365	1104
aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg gat Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val Asp 370 375 380	1152
ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc ttc Leu Ser Val Met Glu Asp His Ser His Phe Asp Ile Lys Pro Phe 385 390 395 400	1200
act act gtt gac ttc tcc agc att tct act cca cat tac gaa gac att Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp Ile 405 410 415	1248

cca ttc aca aga aca gat cca gtg gtt gca gat tac aag tat gac ctg Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu 420 425 430	1296
aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct gca tct cca Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro 435 440 445	1344
cct tat tat tct gag aag act cag ctc tac aat aag cct cat gaa gag Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu 450 455 460	1392
cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat aaa Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys 465 470 475 480	1440
gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga tgc aag ggt Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly 485 490 495	1488
ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt gat Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp 500 505 510	1536
ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac tgt Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys 515 520 525	1584
cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc agg Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile Arg 530 535 540	1632
ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag atc Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile 545 550 555 560	1680
tcc agt gat atc gac cag ctg aat cca gag tcc gct gac ctc cgg gcc Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala 565 570 575	1728
ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg acc Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr 580 585 590	1776
aaa gca aag gcg agg gcg atc ttg aca gga aag aca aca gac aaa tca Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Asp Lys Ser 595 600 605	1824
cca ttc gtt atc tat gac atg aat tcc tta atg atg gga gaa gat aaa Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys 610 615 620	1872
atc aag ttc aaa cac atc acc ccc ctg cag gag cag agc aaa gag gtg Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val 625 630 635 640	1920

gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct gtc Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val 645 650 655	1968
cag gag atc aca gag tat gcc aaa agc att cct ggt ttt gta aat ctt Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu 660 665 670	2016
gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac gag atc Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile 675 680 685	2064
att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc ata Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile 690 695 700	2112
tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg cga Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg 705 710 715 720	2160
aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg aag Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys 725 730 735	2208
ttc aat gca ctg gaa tta gat gac agc gac ttg gca ata ttt att gct Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala 740 745 750	2256
gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag ccc Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro 755 760 765	2304
att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc cag ctg Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu 770 775 780	2352
aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc cag Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln 785 790 795 800	2400
aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag cta ctg Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu 805 810 815	2448
cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg ctc ctg Gln Val Ile Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu Leu 820 825 830	2496
cag gag atc tac aag gac ttg tac tag Gln Glu Ile Tyr Lys Asp Leu Tyr * 835 840	2523

<210> 4  
<211> 840  
<212> PRT

<213> Homo Sapiens

<400> 4

Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu  
1 5 10 15  
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
20 25 30  
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
35 40 45  
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
50 55 60  
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
65 70 75 80  
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
85 90 95  
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu  
100 105 110  
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
115 120 125  
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
130 135 140  
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
145 150 155 160  
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
165 170 175  
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
180 185 190  
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
195 200 205  
Ser Ile Asp Ser Gln Ser Ser Ser Gly Pro Arg Lys His Leu Arg  
210 215 220  
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe  
225 230 235 240  
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys  
245 250 255  
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp  
260 265 270  
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn  
275 280 285  
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro  
290 295 300  
Leu Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Thr  
305 310 315 320  
Pro Cys Ser Leu Ser Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly  
325 330 335  
Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr  
340 345 350  
Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp  
355 360 365  
Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val Asp  
370 375 380  
Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro Phe  
385 390 395 400  
Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp Ile  
405 410 415  
Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu

420	425	430
Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro		
435	440	445
Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu		
450	455	460
Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys		
465	470	475
Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly		
485	490	495
Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp		
500	505	510
Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys		
515	520	525
Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile Arg		
530	535	540
Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile		
545	550	555
Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala		
565	570	575
Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr		
580	585	590
Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser		
595	600	605
Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys		
610	615	620
Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val		
625	630	635
Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val		
645	650	655
Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu		
660	665	670
Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile		
675	680	685
Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile		
690	695	700
Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg		
705	710	715
Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys		
725	730	735
Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala		
740	745	750
Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro		
755	760	765
Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu		
770	775	780
Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln		
785	790	795
Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu		
805	810	815
Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu Leu		
820	825	830
Gln Glu Ile Tyr Lys Asp Leu Tyr		
835	840	

<212> DNA  
<213> Homo Sapiens  
  
<220>  
<221> CDS  
<222> (1)...(2625)  
  
<400> 5  
atg cct cac aac tcc atc aga tct ggc cat gga ggg ctg aac cag ctg 48  
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu  
1 5 10 15  
  
gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg gtc cgc cag 96  
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
20 25 30  
  
cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc gac atc tct 144  
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
35 40 45  
  
cgc cag ctc cgc gtc agc cat ggc tgc gtc agc aag atc ctt ggc agg 192  
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
50 55 60  
  
tac tac gag act ggc agc atc cgg cct gga gtg ata ggg ggc tcc aag 240  
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
65 70 75 80  
  
ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg gac tac aaa 288  
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
85 90 95  
  
cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac cgg ctc ctg 336  
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu  
100 105 110  
  
gct gag ggc gtc tgt gac aat gac act gtg ccc agt gtc agc tcc att 384  
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
115 120 125  
  
aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac ctc cct atg 432  
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
130 135 140  
  
gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac acg ctg atc 480  
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
145 150 155 160  
  
ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg gat tcc ctg 528  
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
165 170 175  
  
ggc tcc acc tac tcc atc aat ggg ctc ctg ggc atc gct cag cct ggc 576  
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
180 185 190

agc gac aag agg aaa atg gat gac agt gat cag gat agc tgc cga cta	624		
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu			
195	200	205	
agc att gac tca cag agc agc gga ccc cga aag cac ctt cgc	672		
Ser Ile Asp Ser Gln Ser Ser Ser Gly Pro Arg Lys His Leu Arg			
210	215	220	
acg gat gcc ttc agc cag cac cac ctc gag ccg ctc gag tgc cca ttt	720		
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe			
225	230	235	240
gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc cac acc aaa	768		
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys			
245	250	255	
ggc gag cag ggc ctc tac ccg ctg ccc ttg ctc aac agc acc ctg gac	816		
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp			
260	265	270	
gac ggg aag gcc acc ctg acc cct tcc aac acg cca ctg ggg cgc aac	864		
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn			
275	280	285	
ctc tcg act cac cag acc tac ccc gtg gtg gca gat cct cac tca ccc	912		
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro			
290	295	300	
ttg gcc ata aag cag gaa acc ccc gag gtg tcc agt tct agc tcc acc	960		
Leu Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Thr			
305	310	315	320
cct tgc tct tta tct agc tcc gcc ctt ttg gat ctg cag caa gtc ggc	1008		
Pro Cys Ser Leu Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly			
325	330	335	
tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc tcc gtg tac	1056		
Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr			
340	345	350	
ggg cag ttc acg ggc cag gcc ctc tca ggg cga gag atg gtg ggg	1104		
Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly			
355	360	365	
ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc gga cag ggc	1152		
Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly			
370	375	380	
agc tat gcc tcc tct gcc atc gca ggc atg gtg gca gaa atg acc atg	1200		
Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met			
385	390	395	400
gtt gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc	1248		
Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser			
405	410	415	

gtg gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc aag 1296  
Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys  
420 425 430

ccc ttc act act gtt gac ttc tcc agc att tct act cca cat tac gaa 1344  
Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu  
435 440 445

gac att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag tat 1392  
Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr  
450 455 460

gac ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct gca 1440  
Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala  
465 470 475 480

tct cca cct tat tat tct gag aag act cag ctc tac aat aag cct cat 1488  
Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His  
485 490 495

gaa gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga 1536  
Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly  
500 505 510

gat aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga tgc 1584  
Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys  
515 520 525

aag ggt ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac aga 1632  
Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg  
530 535 540

tgt gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag 1680  
Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln  
545 550 555 560

tac tgt cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc 1728  
Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala  
565 570 575

atc agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg 1776  
Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala  
580 585 590

gag atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac ctc 1824  
Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu  
595 600 605

cgg gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg 1872  
Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro  
610 615 620

ctg acc aaa gca aag gcg agg gcg atc ttg aca gga aag aca aca gac 1920  
Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp  
625 630 635 640

aaa tca cca ttc gtt atc tat gac atg aat tcc tta atg atg gga gaa 1968  
Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu  
645 650 655

gat aaa atc aag ttc aaa cac atc acc ccc ctg cag gag cag agc aaa 2016  
Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys  
660 665 670

gag gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag 2064  
Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu  
675 680 685

gct gtg cag gag atc aca gag tat gcc aaa agc att cct ggt ttt gta 2112  
Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val  
690 695 700

aat ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac 2160  
Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His  
705 710 715 720

gag atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt 2208  
Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val  
725 730 735

ctc ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc 2256  
Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser  
740 745 750

ctg cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct 2304  
Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala  
755 760 765

gtg aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca ata ttt 2352  
Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe  
770 775 780

att gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg 2400  
Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val  
785 790 795 800

aag ccc att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc 2448  
Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu  
805 810 815

cag ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg 2496  
Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu  
820 825 830

ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag 2544  
Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln  
835 840 845

cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg 2592  
Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro  
850 855 860

ctc ctg cag gag atc tac aag gac ttg tac tag  
Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr \*  
865 870

2625

<210> 6  
<211> 874  
<212> PRT  
<213> Homo Sapiens

<400> 6  
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu  
1 5 10 15  
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
20 25 30  
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
35 40 45  
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
50 55 60  
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
65 70 75 80  
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
85 90 95  
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu  
100 105 110  
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
115 120 125  
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
130 135 140  
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
145 150 155 160  
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
165 170 175  
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
180 185 190  
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
195 200 205  
Ser Ile Asp Ser Gln Ser Ser Ser Gly Pro Arg Lys His Leu Arg  
210 215 220  
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe  
225 230 235 240  
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys  
245 250 255  
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp  
260 265 270  
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn  
275 280 285  
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro  
290 295 300  
Leu Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Thr  
305 310 315 320  
Pro Cys Ser Leu Ser Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly  
325 330 335  
Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr  
340 345 350  
Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly

355	360	365
Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly		
370	375	380
Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met		
385	390	395
400		
Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser		
405	410	415
Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys		
420	425	430
Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu		
435	440	445
Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr		
450	455	460
Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala		
465	470	475
480		
Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His		
485	490	495
Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly		
500	505	510
Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys		
515	520	525
Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg		
530	535	540
Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln		
545	550	555
560		
Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala		
565	570	575
Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala		
580	585	590
Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu		
595	600	605
Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro		
610	615	620
Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp		
625	630	635
640		
Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu		
645	650	655
Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys		
660	665	670
Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu		
675	680	685
Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val		
690	695	700
Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His		
705	710	715
720		
Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val		
725	730	735
Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser		
740	745	750
Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala		
755	760	765
Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe		
770	775	780
Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val		
785	790	795
800		
Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu		

805 810 815  
Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu  
820 825 830  
Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln  
835 840 845  
Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro  
850 855 860  
Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
865 870

<210> 7  
<211> 42  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (3) . . . (41)

<400> 7

ag acc tac ccc gtg gtg gca gaa atg acc atg gtt gac aca g  
Thr Tyr Pro Val Val Ala Glu Met Thr Met Val Asp Thr  
1 5 10

42

<210> 8  
<211> 13  
<212> PRT  
<213> Homo Sapiens

<400> 8

Thr Tyr Pro Val Val Ala Glu Met Thr Met Val Asp Thr  
1 5 10

<210> 9  
<211> 42  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (3) . . . (41)

<400> 9

cg ggc cag gcc ctc ctc tca gaa atg acc atg gtt gac aca g  
Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp Thr  
1 5 10

42

<210> 10  
<211> 13  
<212> PRT  
<213> Homo Sapiens

<400> 10

Gly Gln Ala Leu Leu Ser Glu Met Thr Met Val Asp Thr

1	5	10	
<210> 11			
<211> 42			
<212> DNA			
<213> Homo Sapiens			
<220>			
<221> CDS			
<222> (3) ... (41)			
<400> 11			
cc atc gca ggc atg gtg gca gaa atg acc atg gtt gac aca g			42
Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr			
1	5	10	
<210> 12			
<211> 13			
<212> PRT			
<213> Homo Sapiens			
<400> 12			
Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr			
1	5	10	
<210> 13			
<211> 2711			
<212> DNA			
<213> Homo Sapiens			
<220>			
<221> CDS			
<222> (11) ... (1363)			
<400> 13			
gaattcggcg atg cct cac aac tcc atc aga tct ggc cat gga ggg ctg			49
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu			
1	5	10	
aac cag ctg gga ggg gcc ttt gtg aat ggc aga cct ctg ccg gaa gtg			97
Asn Gln Leu Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val			
15	20	25	
gtc cgc cag cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc			145
Val Arg Gln Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys			
30	35	40	45
gac atc tct cgc cag ctc cgc gtc agc cat ggt tgc gtc agc aag atc			193
Asp Ile Ser Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile			
50	55	60	
ctt ggc agg tac tac gag act ggc agc atc cgg cct gga gtg ata ggg			241
Leu Gly Arg Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly			
65	70	75	

ggc tcc aag ccc aag gtg gcc acc ccc aag gtg gtg gag aag att ggg Gly Ser Lys Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly	289
80 85 90	
gac tac aaa cgc cag aac cct acc atg ttt gcc tgg gag atc cga gac Asp Tyr Lys Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp	337
95 100 105	
cgg ctc ctg gct gag ggc gtc tgg gac aat gac act gtg ccc agt gtc Arg Leu Leu Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val	385
110 115 120 125	
agc tcc att aat aga atc atc cgg acc aaa gtg cag caa cca ttc aac Ser Ser Ile Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn	433
130 135 140	
ctc cct atg gac agc tgc gtg gcc acc aag tcc ctg agt ccc gga cac Leu Pro Met Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His	481
145 150 155	
acg ctg atc ccc agc tca gct gta act ccc ccg gag tca ccc cag tcg Thr Leu Ile Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser	529
160 165 170	
gat tcc ctg ggc tcc acc tac tcc atc aat ggg ctc ctg ggc atc gct Asp Ser Leu Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala	577
175 180 185	
cag cct ggc agc gac aag agg aaa atg gat gac agt gat cag gat agc Gln Pro Gly Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser	625
190 195 200 205	
tgc cga cta agc att gac tca cag agc agc agc gga ccc cga aag Cys Arg Leu Ser Ile Asp Ser Gln Ser Ser Ser Gly Pro Arg Lys	673
210 215 220	
cac ctt cgc acg gat gcc ttc agc cag cac cac ctc gag ccg ctc gag His Leu Arg Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu	721
225 230 235	
tgc cca ttt gag cgg cag cac tac cca gag gcc tat gcc tcc ccc agc Cys Pro Phe Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser	769
240 245 250	
cac acc aaa ggc gag cag ggc ctc tac ccg ctg ccc ttg ctc aac agc His Thr Lys Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser	817
255 260 265	
acc ctg gac gac ggg aag gcc acc ctg acc cct tcc aac acg cca ctg Thr Leu Asp Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu	865
270 275 280 285	
ggg cgc aac ctc tcg act cac cag acc tac ccc gtg gtg gca gat cct Gly Arg Asn Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro	913
290 295 300	

cac tca ccc ttc gcc ata aag cag gaa acc ccc gag gtg tcc agt tct His Ser Pro Phe Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser 305 310 315	961
agc tcc acc cct tcc tct tta tct agc tcc gcc ttt ttg gat ctg cag Ser Ser Thr Pro Ser Ser Leu Ser Ser Ala Phe Leu Asp Leu Gln 320 325 330	1009
caa gtc ggc tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc Gln Val Gly Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala 335 340 345	1057
tcc gtg tac ggg cag ttc acg ggc cag gcc ctc ctc tca ggg cga gag Ser Val Tyr Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu 350 355 360 365	1105
atg gtg ggg ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc Met Val Gly Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser 370 375 380	1153
gga cag ggc agc tat gcc tcc tct gcc atc gca ggc atg gtg gca gga Gly Gln Gly Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly 385 390 395	1201
agt gaa tac tct ggc aat gcc tat ggc cac acc ccc tac tcc tcc tac Ser Glu Tyr Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr 400 405 410	1249
agc gag gcc tgg cgc ttc ccc aac tcc agc ttg ctg agt tcc cca tat Ser Glu Ala Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr 415 420 425	1297
tat tac agt tcc aca tca agg ccg agt gca ccg ccc acc act gcc acg Tyr Tyr Ser Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr 430 435 440 445	1345
gcc ttt gac cat ctg tag ttgaagctt Ala Phe Asp His Leu *	1372
450	

<210> 14  
<211> 450  
<212> PRT  
<213> Homo Sapiens

<400> 14  
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu  
1 5 10 15  
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
20 25 30  
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
35 40 45  
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
50 55 60  
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys

65	70	75	80
Pro Lys Val Ala Thr Pro Lys Val Val	Glu Lys Ile Gly Asp Tyr Lys		
85	90	95	
Arg Gln Asn Pro Thr Met Phe Ala Trp	Glu Ile Arg Asp Arg	Leu	Leu
100	105	110	
Ala Glu Gly Val Cys Asp Asn Asp	Thr Val Pro Ser Val	Ser Ser Ile	
115	120	125	
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln	Pro Phe Asn Leu Pro	Met	
130	135	140	
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser	Pro Gly His Thr	Leu Ile	
145	150	155	160
Pro Ser Ser Ala Val Thr Pro Pro Glu	Ser Pro Gln Ser Asp	Ser Leu	
165	170	175	
Gly Ser Thr Tyr Ser Ile Asn Gly	Leu Leu Gly Ile Ala Gln	Pro Gly	
180	185	190	
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp	Gln Asp Ser Cys Arg	Leu	
195	200	205	
Ser Ile Asp Ser Gln Ser Ser Ser	Gly Pro Arg Lys His	Leu Arg	
210	215	220	
Thr Asp Ala Phe Ser Gln His His	Leu Glu Pro Leu Glu Cys	Pro Phe	
225	230	235	240
Glu Arg Gln His Tyr Pro Glu Ala Tyr	Ala Ser Pro Ser His	Thr Lys	
245	250	255	
Gly Glu Gln Gly Leu Tyr Pro Leu Pro	Leu Leu Asn Ser Thr	Leu Asp	
260	265	270	
Asp Gly Lys Ala Thr Leu Thr Pro Ser	Asn Thr Pro Leu Gly	Arg Asn	
275	280	285	
Leu Ser Thr His Gln Thr Tyr Pro Val	Val Ala Asp Pro His	Ser Pro	
290	295	300	
Phe Ala Ile Lys Gln Glu Thr Pro Glu	Val Ser Ser Ser Ser	Thr	
305	310	315	320
Pro Ser Ser Leu Ser Ser Ala Phe	Leu Asp Leu Gln Gln	Val Gly	
325	330	335	
Ser Gly Val Pro Pro Phe Asn Ala Phe	Pro His Ala Ala Ser	Val Tyr	
340	345	350	
Gly Gln Phe Thr Gly Gln Ala Leu Leu	Ser Gly Arg Glu Met	Val Gly	
355	360	365	
Pro Thr Leu Pro Gly Tyr Pro Pro His	Ile Pro Thr Ser Gly	Gln Gly	
370	375	380	
Ser Tyr Ala Ser Ser Ala Ile Ala Gly	Met Val Ala Gly	Ser Glu Tyr	
385	390	395	400
Ser Gly Asn Ala Tyr Gly His Thr Pro	Tyr Ser Ser Tyr Ser	Glu Ala	
405	410	415	
Trp Arg Phe Pro Asn Ser Ser Leu Leu	Ser Pro Tyr Tyr	Tyr Ser	
420	425	430	
Ser Thr Ser Arg Pro Ser Ala Pro Pro	Thr Thr Ala Thr Ala	Phe Asp	
435	440	445	
His Leu			
450			

<210> 15  
<211> 1608  
<212> DNA  
<213> Homo Sapiens

<220>



<221> CDS  
<222> (91) ... (1608)

<400> 15	tccgggtttt ttcttttaac ggattgatct tttgctagat agagacaaaa tatcagtgtg aattacagca aacccttatt ccatgctgtt atg ggt gaa act ctg gga gat tct Met Gly Glu Thr Leu Gly Asp 1 5	60 114
	cct att gac cca gaa agc gat tcc ttc act gat aca ctg tct gca aac Ser	162
	ata tca caa gaa atg acc atg gtt gac aca gag atg cca ttc tgg ccc Pro Ile Asp Pro Glu Ser Asp Ser Phe Thr Asp Thr Leu Ser Ala Asn 10 15 20	210
	acc aac ttt ggg atc agc tcc gtg gat ctc tcc gta atg gaa gac cac Ile Ser Gln Glu Met Thr Met Val Asp Thr Glu Met Pro Phe Trp Pro 25 30 35 40	258
	tcc cac tcc ttt gat atc aag ccc ttc act act gtt gac ttc tcc agc Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His 45 50 55	306
	att tct act cca cat tac gaa gac att cca ttc aca aga aca gat cca Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser Ser 60 65 70	354
	gtg gtt gca gat tac aag tat gac ctg aaa ctt caa gag tac caa agt Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro 75 80 85	402
	gca atc aaa gtg gag cct gca tct cca cct tat tat tct gag aag act Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser 90 95 100	450
	cag ctc tac aat aag cct cat gaa gag cct tcc aac tcc ctc atg gca Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr 105 110 115 120	498
	att gaa tgt cgt gtc tgt gga gat aaa gct tct gga ttt cac tat gga Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser Asn Ser Leu Met Ala 125 130 135	546
	gtt cat gct tgt gaa gga tgc aag ggt ttc ttc cgg aga aca atc aga Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Gly 140 145 150	594
	ttg aag ctt atc tat gac aga tgt gat ctt aac tgt cgg atc cac aaa Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg 155 160 165	642
	aaa agt aga aat aaa tgt cag tac tgt cgg ttt cag aaa tgc ctt gca Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn Cys Arg Ile His Lys 170 175 180	690

gtg ggg atg tct cat aat gcc atc agg ttt ggg cg <sup>g</sup> atg cca cag gcc	738
Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala	
185 190 195 200	
gag aag gag aag ctg ttg g <sup>c</sup> g <sup>g</sup> gag atc tcc agt gat atc gac cag ctg	786
Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Gln Ala	
205 210 215	
aat cca gag tcc gct gac ctc cgg gcc ctg gca aaa cat ttg tat gac	834
Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu	
220 225 230	
tca tac ata aag tcc ttc ccg ctg acc aaa gca aag g <sup>c</sup> g <sup>g</sup> agg g <sup>c</sup> g <sup>g</sup> atc	882
Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp	
235 240 245	
ttg aca gga aag aca aca gac aaa tca cca ttc gtt atc tat gac atg	930
Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile	
250 255 260	
aat tcc tta atg atg gga gaa gat aaa atc aag ttc aaa cac atc acc	978
Leu Thr Gly Lys Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met	
265 270 275 280	
ccc ctg cag gag ca <sup>g</sup> a <sup>g</sup> g <sup>c</sup> g <sup>t</sup> g <sup>c</sup> atc cgc atc ttt ca <sup>g</sup> gg <sup>c</sup>	1026
Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr	
285 290 295	
tgc cag ttt cgc tcc gtg gag g <sup>c</sup> t g <sup>t</sup> cag gag atc aca gag tat g <sup>c</sup> c	1074
Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly	
300 305 310	
aaa agc att cct ggt ttt gta aat ctt gac ttg aac gac caa gta act	1122
Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala	
315 320 325	
ctc ctc aaa tat gga gtc cac gag atc att tac aca atg ctg g <sup>c</sup> c tcc	1170
Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr	
330 335 340	
ttg atg aat aaa gat ggg gtt ctc ata tcc gag gg <sup>c</sup> caa gg <sup>c</sup> ttc atg	1218
Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser	
345 350 355 360	
aca agg gag ttt cta aag agc ctg cga aag cct ttt ggt gac ttt atg	1266
Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met	
365 370 375	
gag ccc aag ttt gag ttt g <sup>c</sup> t g <sup>t</sup> a <sup>g</sup> g <sup>t</sup> aat gca ctg gaa tta gat	1314
Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met	
380 385 390	
gac agc gac ttg gca ata ttt att g <sup>c</sup> t g <sup>t</sup> c att att ctc agt gga gac	1362
Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp	
395 400 405	

cgc cca ggt ttg ctg aat gtg aag ccc att gaa gac att caa gac aac 1410  
Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp  
410 415 420

ctg cta caa gcc ctg gag ctc cag ctg aag ctc aac cac cct gag tcc 1458  
Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn  
425 430 435 440

tca cag ctg ttt gcc aag ctg ctc cag aaa atg aca gac ctc aga cag 1506  
Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser  
445 450 455

att gtc acg gaa cac gtg cag cta ctg cag gtg atc aag aag acg gag 1554  
Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln  
460 465 470

aca gac atg agt ctt cac ccg ctc ctg cag gag atc tac aag gac ttg 1602  
Ile Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu  
475 480 485

tac tag 1608  
Thr Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu  
490 495 500

<210> 16  
<211> 505  
<212> PRT  
<213> Homo Sapiens

<400> 16  
Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser  
1 5 10 15  
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val  
20 25 30  
Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val  
35 40 45  
Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro  
50 55 60  
Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp  
65 70 75 80  
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp  
85 90 95  
Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser  
100 105 110  
Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu  
115 120 125  
Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp  
130 135 140  
Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys  
145 150 155 160  
Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys  
165 170 175  
Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr  
180 185 190

Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile  
195 200 205  
Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu  
210 215 220  
Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg  
225 230 235 240  
Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu  
245 250 255  
Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys  
260 265 270  
Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp  
275 280 285  
Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu  
290 295 300  
Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala  
305 310 315 320  
Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn  
325 330 335  
Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu  
340 345 350  
Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu  
355 360 365  
Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu  
370 375 380  
Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val  
385 390 395 400  
Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile  
405 410 415  
Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys  
420 425 430  
Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln  
435 440 445  
Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu  
450 455 460  
Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu  
465 470 475 480  
Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu  
485 490 495  
Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
500 505

<210> 17  
<211> 21  
<212> DNA  
<213> Homo Sapiens

<400> 17  
gcattgactc acagagcagc a

21

<210> 18  
<211> 18  
<212> DNA  
<213> Homo Sapiens

<400> 18  
gctcaacagc accctgga

18

<210> 19  
<211> 20  
<212> DNA  
<213> Homo Sapiens

<400> 19  
gcaacctctc gactcaccag 20

<210> 20  
<211> 20  
<212> DNA  
<213> Homo Sapiens

<400> 20  
caaaggagtg ggagtggtct 20

<210> 21  
<211> 20  
<212> DNA  
<213> Homo Sapiens

<400> 21  
cattacggag agatccacgg 20

<210> 22  
<211> 2596  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (161) ... (2596)

<400> 22  
ttcagaagga ggagagacac cggggccagg gcaccctcgc gggcgccgg acccaagg 60  
tgagggcctg cagccggccg gccagggcag cggcaggcgc ggcccgacc tacggagga 120  
agcccccggc cctccggccgg ctgcgagcga ctcccccggcgt atg cct cac aac tcc 175  
Met Pro His Asn  
1

atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg 223  
Ser  
5

aat ggc aga cct ctg ccg gaa gtg gtc cgc cag cgc atc gta gac ctg 271  
Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu Gly Gly Ala Phe Val  
10 15 20

gcc cac cag ggt gta agg ccc tgc gac atc tct cgc cag ctc cgc gtc 319  
Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu  
25 30 35

agc cat ggc tgc gtc agc aag atc ctt ggc agg tac tac gag act ggc 367  
Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val  
40 45 50

agc atc cgg cct gga gtg ata ggg ggc tcc aag ccc aag gtg gcc acc		415
Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg Tyr Tyr Glu Thr Gly		
55	60	65
ccc aag gtg gtg gag aag att ggg gac tac aaa cgc cag aac cct acc		463
Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys Pro Lys Val Ala Thr		
70	75	80
atg ttt gcc tgg gag atc cga gac cgg ctc ctg gct gag ggc gtc tgt		511
Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys Arg Gln Asn Pro Thr		
90	95	100
gac aat gac act gtg ccc agt gtc agc tcc att aat aga atc atc cgg		559
Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu Ala Glu Gly Val Cys		
105	110	115
acc aaa gtg cag caa cca ttc aac ctc cct atg gac agc tgc gtg gcc		607
Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile Asn Arg Ile Ile Arg		
120	125	130
acc aag tcc ctg agt ccc gga cac acg ctg atc ccc agc tca gct gta		655
Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met Asp Ser Cys Val Ala		
135	140	145
act ccc ccg gag tca ccc cag tcg gat tcc ctg ggc tcc acc tac tcc		703
Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile Pro Ser Ser Ala Val		
150	155	160
165		
atc aat ggg ctc ctg ggc atc gct cag cct ggc agc gac aag agg aaa		751
Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu Gly Ser Thr Tyr Ser		
170	175	180
atg gat gac agt gat cag gat agc tgc cga cta agc att gac tca cag		799
Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly Ser Asp Lys Arg Lys		
185	190	195
agc agc agc gga ccc cga aag cac ctt cgc acg gat gcc ttc agc		847
Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu Ser Ile Asp Ser Gln		
200	205	210
cag cac cac ctc gag ccg ctc gag tgc cca ttt gag cgg cag cac tac		895
Ser Ser Ser Gly Pro Arg Lys His Leu Arg Thr Asp Ala Phe Ser		
215	220	225
cca gag gcc tat gcc ccc agc cac acc aaa ggc gag cag ggc ctc		943
Gln His His Leu Glu Pro Leu Glu Cys Pro Phe Glu Arg Gln His Tyr		
230	235	240
245		
tac ccg ctg ccc ttg ctc aac agc acc ctg gac gac ggg aag gcc acc		991
Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys Gly Glu Gln Gly Leu		
250	255	260
ctg acc cct tcc aac acg cca ctg ggg cgc aac ctc tcg act cac cag		1039
Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp Asp Gly Lys Ala Thr		
265	270	275

acc tac ccc gtg gtg gca ggg cga gag atg gtg ggg ccc acg ctg ccc			1087
Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn Leu Ser Thr His Gln			
280	285	290	
gga tac cca ccc cac atc ccc acc agc gga cag ggc agc tat gcc tcc			1135
Thr Tyr Pro Val Val Ala Gly Arg Glu Met Val Gly Pro Thr Leu Pro			
295	300	305	
tct gcc atc gca ggc atg gtg gca gaa atg acc atg gtt gac aca gag			1183
Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser			
310	315	320	325
atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg gat ctc tcc			1231
Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr Glu			
330	335	340	
gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc ttc act act			1279
Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser			
345	350	355	
gtt gac ttc tcc agc att tct act cca cat tac gaa gac att cca ttc			1327
Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr			
360	365	370	
aca aga aca gat cca gtg gtt gca gat tac aag tat gac ctg aaa ctt			1375
Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe			
375	380	385	
caa gag tac caa agt gca atc aaa gtg gag cct gca tct cca cct tat			1423
Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu			
390	395	400	405
tat tct gag aag act cag ctc tac aat aag cct cat gaa gag cct tcc			1471
Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr			
410	415	420	
aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat aaa gct tct			1519
Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser			
425	430	435	
gga ttt cac tat gga gtt cat gct tgt gaa gga tgc aag ggt ttc ttc			1567
Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser			
440	445	450	
cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt gat ctt aac			1615
Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe			
455	460	465	
tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac tgt cgg ttt			1663
Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn			
470	475	480	485
cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc agg ttt ggg			1711
Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe			
490	495	500	

cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag atc tcc agt Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile Arg Phe Gly 505	510	515	1759	
gat atc gac cag ctg aat cca gag tcc gct gac ctc cgg gcc ctg gca Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser 520	525	530	1807	
aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg acc aaa gca Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala 535	540	545	1855	
aag gcg agg gcg atc ttg aca gga aag aca aca gac aaa tca cca ttc Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala 550	555	560	565	1903
gtt atc tat gac atg aat tcc tta atg atg gga gaa gat aaa atc aag Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe 570	575	580	1951	
ttc aaa cac atc acc ccc ctg cag gag cag agc aaa gag gtg gcc atc Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys 585	590	595	1999	
cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct gtg cag gag Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile 600	605	610	2047	
atc aca gag tat gcc aaa agc att cct ggt ttt gta aat ctt gac ttg Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu 615	620	625	2095	
aac gac caa gta act ctc ctc aaa tat gga gtc cac gag atc att tac Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu 630	635	640	645	2143
aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc ata tcc gag Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr 650	655	660	2191	
ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg cga aag cct Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu 665	670	675	2239	
ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg aag ttc aat Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro 680	685	690	2287	
gca ctg gaa tta gat gac agc gac ttg gca ata ttt att gct gtc att Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn 695	700	705	2335	
att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag ccc att gaa Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile 710	715	720	725	2383

gac att caa gac aac ctg cta caa gcc ctg gag ctc cag ctg aag ctg 2431  
Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu  
730 735 740

aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc cag aaa atg 2479  
Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu  
745 750 755

aca gac ctc aga cag att gtc acg gaa cac gtg cag cta ctg cag gtg 2527  
Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met  
760 765 770

atc aag aag acg gag aca gac atg agt ctt cac ccg ctc ctg cag gag 2575  
Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu Leu Gln Val  
775 780 785

atc tac aag gac ttg tac tag 2596  
Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu Leu Gln Glu  
790 795 800 805

<210> 23  
<211> 811  
<212> PRT  
<213> Homo Sapiens

<400> 23  
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu  
1 5 10 15  
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
20 25 30  
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
35 40 45  
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
50 55 60  
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
65 70 75 80  
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
85 90 95  
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu  
100 105 110  
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
115 120 125  
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
130 135 140  
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
145 150 155 160  
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
165 170 175  
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
180 185 190  
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
195 200 205  
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg  
210 215 220

Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe  
225 230 235 240  
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys  
245 250 255  
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp  
260 265 270  
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn  
275 280 285  
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Gly Arg Glu Met Val  
290 295 300  
Gly Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln  
305 310 315 320  
Gly Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr  
325 330 335  
Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser  
340 345 350  
Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile  
355 360 365  
Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr  
370 375 380  
Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys  
385 390 395 400  
Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro  
405 410 415  
Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro  
420 425 430  
His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys  
435 440 445  
Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly  
450 455 460  
Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp  
465 470 475 480  
Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys  
485 490 495  
Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn  
500 505 510  
Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu  
515 520 525  
Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp  
530 535 540  
Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe  
545 550 555 560  
Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr  
565 570 575  
Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly  
580 585 590  
Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser  
595 600 605  
Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val  
610 615 620  
Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe  
625 630 635 640  
Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val  
645 650 655  
His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly  
660 665 670

Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys  
675 680 685  
Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe  
690 695 700  
Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile  
705 710 715 720  
Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn  
725 730 735  
Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu  
740 745 750  
Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys  
755 760 765  
Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val  
770 775 780  
Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His  
785 790 795 800  
Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
805 810

<210> 24  
<211> 2711  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (161) ... (1510)

<400> 24

ttcagaagga ggagagacac cggggccagg gcaccctcgc gggcgggcg acccaagcag 60  
tgagggcctg cagccggccg gccagggcag cggcaggcgc ggcccgacc tacgggagga 120  
agcccccagc cctcggcggg ctgcgagcga ctccccggcg atg cct cac aac tcc 175  
Met Pro His Asn Ser  
1 5

atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg 223  
Ile Arg Ser Gly His Gly Leu Asn Gln Leu Gly Gly Ala Phe Val  
10 15 20

aat ggc aga cct ctg ccg gaa gtg gtc cgc cag cgc atc gta gac ctg 271  
Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu  
25 30 35

gcc cac cag ggt gta agg ccc tgc gac atc tct cgc cag ctc cgc gtc 319  
Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val  
40 45 50

agc cat ggc tgc gtc agc aag atc ctt ggc agg tac tac gag act ggc 367  
Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg Tyr Tyr Glu Thr Gly  
55 60 65

agc atc cgg cct gga gtg ata ggg ggc tcc aag ccc aag gtg gcc acc 415  
Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys Pro Lys Val Ala Thr  
70 75 80 85

ccc aag gtg gtg gag aag att ggg gac tac aaa cgc cag aac cct acc 463

Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys Arg Gln Asn Pro Thr			
90	95	100	
atg ttt gcc tgg gag atc cga gac cgg ctc ctg gct gag ggc gtc tgt			511
Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu Ala Glu Gly Val Cys			
105	110	115	
gac aat gac act gtg ccc agt gtc agc tcc att aat aga atc atc cgg			559
Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile Asn Arg Ile Ile Arg			
120	125	130	
acc aaa gtg cag caa cca ttc aac ctc cct atg gac agc tgc gtg gcc			607
Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met Asp Ser Cys Val Ala			
135	140	145	
acc aag tcc ctg agt ccc gga cac acg ctg atc ccc agc tca gct gta			655
Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile Pro Ser Ser Ala Val			
150	155	160	165
act ccc ccg gag tca ccc cag tcg gat tcc ctg ggc tcc acc tac tcc			703
Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu Gly Ser Thr Tyr Ser			
170	175	180	
atc aat ggg ctc ctg ggc atc gct cag cct ggc agc gac aag agg aaa			751
Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly Ser Asp Lys Arg Lys			
185	190	195	
atg gat gac agt gat cag gat agc tgc cga cta agc att gac tca cag			799
Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu Ser Ile Asp Ser Gln			
200	205	210	
agc agc agc gga ccc cga aag cac ctt cgc acg gat gcc ttc agc			847
Ser Ser Ser Gly Pro Arg Lys His Leu Arg Thr Asp Ala Phe Ser			
215	220	225	
cag cac cac ctc gag ccg ctc gag tgc cca ttt gag cgg cag cac tac			895
Gln His His Leu Glu Pro Leu Glu Cys Pro Phe Glu Arg Gln His Tyr			
230	235	240	245
cca gag gcc tat gcc tcc ccc agc cac acc aaa ggc gag cag ggc ctc			943
Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys Gly Glu Gln Gly Leu			
250	255	260	
tac ccg ctg ccc ttg ctc aac agc acc ctg gac gac ggg aag gcc acc			991
Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp Asp Gly Lys Ala Thr			
265	270	275	
ctg acc cct tcc aac acg cca ctg ggg cgc aac ctc tcg act cac cag			1039
Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn Leu Ser Thr His Gln			
280	285	290	
acc tac ccc gtg gtg gca gat cct cac tca ccc ttg gcc ata aag cag			1087
Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro Leu Ala Ile Lys Gln			
295	300	305	
gaa acc ccc gag gtg tcc agt tct agc tcc acc cct tgc tct tta tct			1135

Glu Thr Pro Glu Val Ser Ser Ser Ser Ser Thr Pro Cys Ser Leu Ser  
310 315 320 325  
agc tcc gcc ctt ttg gat ctg cag caa gtc ggc tcc ggg gtc ccg ccc 1183  
Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly Ser Gly Val Pro Pro  
330 335 340  
ttc aat gcc ttt ccc cat gct gcc tcc gtg tac ggg cag ttc acg ggc 1231  
Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr Gly Gln Phe Thr Gly  
345 350 355  
cag gcc ctc ctc tca ggg cga gag atg gtg ggg ccc acg ctg ccc gga 1279  
Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly Pro Thr Leu Pro Gly  
360 365 370  
tac cca ccc cac atc ccc acc agc gga cag ggc agc tat gcc tcc tct 1327  
Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser Ser  
375 380 385  
gcc atc gca ggc atg gtg gca gga agt gaa tac tct ggc aat gcc tat 1375  
Ala Ile Ala Gly Met Val Ala Gly Ser Glu Tyr Ser Gly Asn Ala Tyr  
390 395 400 405  
ggc cac acc ccc tac tcc tcc tac agc gag gcc tgg ggc ttc ccc aac 1423  
Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala Trp Gly Phe Pro Asn  
410 415 420  
tcc agc ttg ctg agt tcc cca tat tat tac agt tcc aca tca agg ccg 1471  
Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Ser Ser Thr Ser Arg Pro  
425 430 435  
agt gca ccg ccc acc act gcc acg gcc ttt gac cat ctg tagttgccat 1520  
Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp His Leu  
440 445 450  
ggggacagtg ggagcgactg agcaacagga ggactcagcc tgggacaggc cccagaggt 1580  
cacacaaaagg aatctttatt attacatgaa aaataaccac aagtccagca ttgcggcaca 1640  
ctccctgtgt ggttaattta atgaaccatg aaagacagga tgacccttggca caaggccaaa 1700  
ctgtcctcca agactcctta atgaggggca ggagtccocag ggaaagagaa ccatgcccatt 1760  
ctgaaaaaga caaaaattgaa gaagaaatgt agccccagcc ggtaccctcc aaaggagaga 1820  
agaagaata gccgaggaac ttggggggat ggcgaatggc ttctgcccgg gcccaagggt 1880  
gcacagggca cctccatggc tccattatta acacaactct agcaattatg gaccataagc 1940  
acttcctcc agccccacaag tcacagcctg gtgccgaggc tctgctcacc agccacccag 2000  
ggagtcaccc ccctcagcct cccgcctgcc ccacacggag gctctggctg ttctcttcc 2060  
tccactccat ttgcttggct ttcttacac tccctcttgc gatgggctga gggctggagc 2120  
gagtcctca gaaattccac caggctgtca gctgaccctt ttttcttgc gctgtgaagg 2180  
tatagcacca cccaggtctt cctgcagtgc ggcattccct tggcagctgc cgtcagccag 2240  
gccagccccca gggagcttaa aacagacatt ccacagggcc tggcccccctg ggaggtgagg 2300  
tgtgggtgtc ggcttcaccc agggcagaac aaggcagaat cgcaaggaaac ccgcttcccc 2360  
ttcctgacag ctcctgccaa gccaaatgtt cttcctgcag ctcacgccc ccagctactg 2420  
aagggaccca aggcacccccc tgaagccagc gatagagggc ccctctctgc tccccagcag 2480  
ctcctgcccc caaggcctga ctgtatatac tgtaaatgaa actttgtttt ggtcaagctt 2540  
ccttccttc aaccccccaga ctttggcctc tgagtgaaat gtctctttt gccctgtggg 2600  
gcttccttc ttgatgctt tttcttttt taaagacaac ctgccattac cacatgactc 2660  
aataaaccat tgctttcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2711

<210> 25  
<211> 450  
<212> PRT  
<213> Homo Sapiens

<400> 25  
Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu  
1 5 10 15  
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln  
20 25 30  
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
35 40 45  
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg  
50 55 60  
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
65 70 75 80  
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
85 90 95  
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu  
100 105 110  
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
115 120 125  
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
130 135 140  
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
145 150 155 160  
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
165 170 175  
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
180 185 190  
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
195 200 205  
Ser Ile Asp Ser Gln Ser Ser Ser Gly Pro Arg Lys His Leu Arg  
210 215 220  
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe  
225 230 235 240  
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys  
245 250 255  
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp  
260 265 270  
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn  
275 280 285  
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro  
290 295 300  
Leu Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Thr  
305 310 315 320  
Pro Cys Ser Leu Ser Ser Ser Ala Leu Leu Asp Leu Gln Gln Val Gly  
325 330 335  
Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr  
340 345 350  
Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly  
355 360 365  
Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly  
370 375 380  
Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly Ser Glu Tyr  
385 390 395 400

Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala  
405 410 415  
Trp Gly Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser  
420 425 430  
Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp  
435 440 445  
His Leu  
450

<210> 26  
<211> 1811  
<212> DNA  
<213> Homo Sapiens

<220>  
<221> CDS  
<222> (173) ... (1609)

<400> 26

ccgacacctac cccaggcgcc cttgacgttg gtcttgcgg caggagacag caccatggtg 60  
ggttctctct gaggctggga attcccgagc ccgagccgca gccggccgcct ggggggcttg 120  
ggtcggccctc gaggacaccc gagagggggcg ccacgcccgt gtcggccgcag aa atg acc 178  
Met Thr  
1

atg gtt gac aca gag atc gca ttc tgg ccc acc aac ttt ggg atc agc 226  
Met Val Asp Thr Glu Ile Ala Phe Trp Pro Thr Asn Phe Gly Ile Ser  
5 10 15

tcc gtg gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc 274  
Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile  
20 25 30

aag ccc ttc act act gtt gac ttc tcc agc att tct act cca cat tac 322  
Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr  
35 40 45 50

gaa gac att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag 370  
Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys  
55 60 65

tat gac ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct 418  
Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro  
70 75 80

gca tct cca cct tat tat tct gag aag act cag ctc tac aat aag cct 466  
Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro  
85 90 95

cat gaa gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt 514  
His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys  
100 105 110

gga gat aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga 562  
Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly  
115 120 125 130

tgc aag ggt ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp 135 140 145	610
aga tgt gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys 150 155 160	658
cag tac tgt cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn 165 170 175	706
gcc atc agg ttt ggg cgg atc gca cag gcc gag aag gag aag ctg ttg Ala Ile Arg Phe Gly Arg Ile Ala Gln Ala Glu Lys Glu Lys Leu Leu 180 185 190	754
gcg gag atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp 195 200 205 210	802
ctc cgt cag gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc Leu Arg Gln Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser 215 220 225	850
ttc ccg ctg acc aaa gca aag gcg agg gcg atc ttg aca gga aag aca Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr 230 235 240	898
aca gac aaa tca cca ttc gtt atc tat gac atg aat tcc tta atg atg Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met 245 250 255	946
gga gaa gat aaa atc aag ttc aaa cac atc acc ccc ctg cag gag cag Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln 260 265 270	994
agc aaa gag gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser 275 280 285 290	1042
gtg gag gct gtg cag gag atc aca gag tat gcc aaa agc att cct ggt Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly 295 300 305	1090
ttt gta aat ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly 310 315 320	1138
gtc cac gag atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp 325 330 335	1186
ggg gtt ctc ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu 340 345 350	1234

aag agc ctg cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag	1282
Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu	
355 360 365 370	
ttt gct gtg aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca	1330
Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala	
375 380 385	
ata ttt att gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg	1378
Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu	
390 395 400	
aat gtg aag ccc att gaa gac att caa gac aac ctg cta caa gcc ctg	1426
Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Gln Ala Leu	
405 410 415	
gag ctc cag ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc	1474
Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala	
420 425 430	
aag ctg ctc cag aaa atg aca gac ctc aga cag att gtc acg gaa cac	1522
Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His	
435 440 445 450	
gtg cag cta ctg cag gtg atc aag aac acg gag aca gac atg agt ctt	1570
Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu	
455 460 465	
cac ccg ctc ctg cag gag atc tac aag gac ttg tac tag cagagagtcc	1619
His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr *	
470 475	
tgagccactg ccaacatttc ccttcttcca gttgcactat tctgagggaa aatctgacca	1679
taagaaattt actgtgaaaa agcgaaaaaa aaagaaaaagg gtttagaata tgatctattt	1739
tatgcattttt gtttataaag acacattac aatttacttt taatattaaa aattaccata	1799
ttatgaaattt gc	1811
<210> 27	
<211> 478	
<212> PRT	
<213> Homo Sapiens	
<400> 27	
Met Thr Met Val Asp Thr Glu Ile Ala Phe Trp Pro Thr Asn Phe Gly	
1 5 10 15	
Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe	
20 25 30	
Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro	
35 40 45	
His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp	
50 55 60	
Tyr Lys Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val	
65 70 75 80	
Glu Pro Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn	
85 90 95	

Lys Pro His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg  
100 105 110  
Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys  
115 120 125  
Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile  
130 135 140  
Tyr Asp Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn  
145 150 155 160  
Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser  
165 170 175  
His Asn Ala Ile Arg Phe Gly Arg Ile Ala Gln Ala Glu Lys Glu Lys  
180 185 190  
Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser  
195 200 205  
Ala Asp Leu Arg Gln Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile  
210 215 220  
Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly  
225 230 235 240  
Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu  
245 250 255  
Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln  
260 265 270  
Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe  
275 280 285  
Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile  
290 295 300  
Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys  
305 310 315 320  
Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn  
325 330 335  
Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu  
340 345 350  
Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys  
355 360 365  
Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp  
370 375 380  
Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly  
385 390 395 400  
Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln  
405 410 415  
Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu  
420 425 430  
Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr  
435 440 445  
Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met  
450 455 460  
Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
465 470 475

<210> 28  
<211> 20  
<212> DNA  
<213> Homo Sapiens

<400> 28  
gccaccaagt ccctgagtcc

<210> 29  
<211> 19  
<212> DNA  
<213> Homo Sapiens

<400> 29  
gacctacggg aggaagccc 19

<210> 30  
<211> 18  
<212> DNA  
<213> Homo Sapiens

<400> 30  
gcggacccaa gcagttag 18

<210> 31  
<211> 21  
<212> DNA  
<213> Homo Sapiens

<400> 31  
tttcttatgg tcagatttc c 21

<210> 32  
<211> 21  
<212> DNA  
<213> Homo Sapiens

<400> 32  
acccagaaag cgattccttc a 21

<210> 33  
<211> 20  
<212> DNA  
<213> Homo Sapiens

<400> 33  
atgggtgaaa ctctgggaga 20

<210> 34  
<211> 20  
<212> DNA  
<213> Homo Sapiens

<400> 34  
ttgctgcaga tccaaaaagg 20

<210> 35  
<211> 20  
<212> DNA  
<213> Homo Sapiens

<400> 35  
gaggaagggg tggagctaga 20

<210> 36  
<211> 537  
<212> DNA  
<213> Homo Saiens

<220>  
<223> n = A or T or C or G or other

<400> 36

atg ggt gaa act ctg gga gat tct cct att gac cca gaa agc gat tcc	48
ttc act gat aca ctg tct gca aac ata tca caa gaa nat cct cac tca	96
ccc ttc gcc ata aag cag gaa acc ccc gag gtg tcc agt tct agc tcc	144
acc cct tcc tct tta tct agc tcc gcc ttt ttg gat ctg cag caa gtc	192
ggc tcc ggg gtc ccg ccc ttc aat gcc ttt ccc cat gct gcc tcc gtg	240
tac ggg cag ttc acg ggc cag gcc ctc ctc tca ggg cga gag atg gtg	288
ggg ccc acg ctg ccc gga tac cca ccc cac atc ccc acc agc gga cag	336
ggc agc tat gcc tcc tct gcc atc gca ggc atg gtg gca gga agt gaa	384
tac tct ggc aat gcc tat ggc cac acc ccc tac tcc tcc tac agc gag	432
gcc tgg cgc ttc ccc aac tcc agc ttg ctg agt tcc cca tat tat tac	480
agt tcc aca tca agg ccg agt gca ccg ccc acc act gcc acg gcc ttt	528
gac cat ctg	537

<210> 37  
<211> 348  
<212> DNA  
<213> Homo Sapiens

<220>  
<223> n = A or T or C or G or other

<400> 37

atgggtgaaa ctctgggaga ttctcctatt gacccagaaa gcgattcctt cactgataca	60
ctgtctgcaa acatatcaca agaanggcga gagatggtgg ggcccacgct gcccggatac	120
ccaccccaaca tccccaccag cggacaggc agctatgcct cctctgccat cgcaggcatg	180
gtggcaggaa gtgaatactc tggcaatgcc tatggccaca cccctactc ctccctacagc	240
gaggcctggc gcttcccaa ctccagcttg ctgagttccc catattatta cagttccaca	300
tcaaggccga gtgcaccgccc caccactgcc acggcctttg accatctg	348

<210> 38  
<211> 246  
<212> DNA  
<213> Homo Sapiens

<220>  
<223> n = A or T or C or G or other

<400> 38

atgggtgaaa ctctgggaga ttctcctatt gacccagaaa gcgattcctt cactgataca	60
ctgtctgcaa acatatcaca agaangaagt gaataactctg gcaatgccta tggccacacc	120
ccctactcct cctacagcga ggcctggcgc ttccccaaact ccagcttgct gagttccca	180
tattattaca gttccacatc aaggccgagt gcaccgccc a ccactgccac ggccttgac	240
catctg	246

<210> 39  
<211> 178

<212> PRT  
<213> Homo Sapiens

<220>  
<223> Xaa = any amino acid

<400> 39  
Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser  
1 5 10 15  
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Xaa Pro His Ser  
20 25 30  
Pro Phe Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser  
35 40 45  
Thr Pro Ser Ser Leu Ser Ser Ala Phe Leu Asp Leu Gln Gln Val  
50 55 60  
Gly Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val  
65 70 75 80  
Tyr Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu Met Val  
85 90 95  
Gly Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln  
100 105 110  
Gly Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly Ser Glu  
115 120 125  
Tyr Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu  
130 135 140  
Ala Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr  
145 150 155 160  
Ser Ser Thr Ser Arg Pro Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp  
165 170 175  
His Leu

<210> 40  
<211> 116  
<212> PRT  
<213> Homo Sapiens

<220>  
<223> Xaa = any amino acid

<400> 40  
Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser  
1 5 10 15  
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Xaa Arg Glu Met  
20 25 30  
Val Gly Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly  
35 40 45  
Gln Gly Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly Ser  
50 55 60  
Glu Tyr Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser  
65 70 75 80  
Glu Ala Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr  
85 90 95  
Tyr Ser Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala  
100 105 110  
Phe Asp His Leu

115

<210> 41  
<211> 82  
<212> PRT  
<213> Homo Sapiens

<220>  
<223> Xaa = any amino acid

<400> 41

Met Gly Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser  
1 5 10 15  
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr  
20 25 30  
Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala  
35 40 45  
Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser  
50 55 60  
Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp  
65 70 75 80  
His Leu

<210> 42  
<211> 43  
<212> DNA  
<213> Homo Sapiens

<220>  
<223> n = A or T or C or G or other

<221> CDS  
<222> (1) ... (43)

<400> 42

tct gca aac ata tca caa gaa nat cct cac tca ccc ttc gcc a  
Ser Ala Asn Ile Ser Gln Glu Xaa Pro His Ser Pro Phe Ala  
1 5 10

43

<210> 43  
<211> 14  
<212> PRT  
<213> Homo Sapiens

<220>  
<223> Xaa = any amino acid

<400> 43

Ser Ala Asn Ile Ser Gln Glu Xaa Pro His Ser Pro Phe Ala  
1 5 10

<210> 44  
<211> 43  
<212> DNA

<213> Homo Sapiens

<220>

<223> n = A or T or C or G or other

<221> CDS

<222> (1) ... (43)

<400> 44

tct gca aac ata tca caa gaa n<sub>g</sub>g cga gag atg gtg ggg ccc a  
Ser Ala Asn Ile Ser Gln Glu Xaa Arg Glu Met Val Gly Pro  
1 5 10

43

<210> 45

<211> 14

<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 45

Ser Ala Asn Ile Ser Gln Glu Xaa Arg Glu Met Val Gly Pro  
1 5 10

<210> 46

<211> 43

<212> DNA

<213> Homo Sapiens

<220>

<223> n = a or T or C or G or other

<221> CDS

<222> (1) ... (43)

<400> 46

tct gca aac ata tca caa gaa a<sub>g</sub>t gaa tac tct ggc aat g  
Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr Ser Gly Asn  
1 5 10

43

<210> 47

<211> 14

<212> PRT

<213> Homo Sapiens

<220>

<223> Xaa = any amino acid

<400> 47

Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr Ser Gly Asn  
1 5 10